STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
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Application Serial Number: *10/642,272*
Source: *1FWO*
Date Processed by STIC: *7/7/05*

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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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Revised 01/24/05

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/642,272

DATE: 07/07/2005
TIME: 12:14:55

Input Set : A:\EP.txt
Output Set: N:\CRF4\07072005\J642272.raw

```
     2 <110> APPLICANT: SUNTORY LIMITED
     3        SUNTORY BIOMEDICAL RESEARCH LIMITED
W--> 4 <120> TITLE OF INVENTION: THERAPEUTIC METHODS AND AGENTS FOR DISEASES ASSOCIATED WITH
W--> 5        DECREASED EXPRESSION OF AOP-1 GENE OR AOP-1
W--> 6 <130> FILE REFERENCE: YCT-687
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/642,272
C--> 7 <141> CURRENT FILING DATE: 2003-08-18
W--> 7 <160> NUMBER OF SEQ ID: 30
```

pp 1-6, 8

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
     9 <210> SEQ ID NO: 1
    10 <211> LENGTH: 1542
E--> 11 <212> TYPE: (mRNA)
    12 <213> ORGANISM: Homo sapiens
OK-> 13 <400> SEQUENCE: 1
    14 ctgaagatgg cggctgctgt aggacggttg ctccgagcgt cggttgcccg acatgtgagt   60
    15 gccattcctt ggggcatttc tgccactgca gccctcaggc ctgctgcatg tggaagaacg  120
    16 agcttgacaa atttattgtg ttctggttcc agtcaagcaa aattattcag caccagttcc  180
    17 tcatgccatg cacctgctgt cacccagcat gcaccctatt ttaagggtac agccgttgtc  240
    18 aatggagagt tcaaagacct aagccttgat gactttaagg ggaaatattt ggtgcttttc  300
    19 ttctatcctt tggatttcac ctttgtgtgt cctacagaaa ttgttgcttt tagtgacaaa  360
    20 gctaacgaat ttcacgatgt gaactgtgaa gttgtcgcag tctcagtgga ttcccacttt  420
    21 agccatcttg cctggataaa tacaccaaga aagaatggtg gtttgggcca catgaacatc  480
    22 gcactcttgt cagacttaac taagcagatt tcccgagact acggtgtgct gttagaaggt  540
    23 tctggtcttg cactaagagg tctcttcata attgacccca atggagtcat caagcatttg  600
    24 agcgtcaacg atctcccagt gggccgaagc gtggaagaaa ccctccgctt ggtgaaggcg  660
    25 ttccagtatg tagaaacaca tggagaagtc tgcccagcga actggacacc ggattctcct  720
    26 acgatcaagc caagtccagc tgcttccaaa gagtactttc agaaggtaaa tcagtagatc  780
    27 acccatgtgt atctgcacct tctcaactga gagaagaacc acagttgaaa cctgctttta  840
    28 tcattttcaa gatggttatt tgtagaaggc aaggaaccaa ttatgcttgt attcataagt  900
    29 attactctaa atgttttgtt tttgtaattc tggctaggac ctttttaaaca tggttagttg  960
    30 ctagtacagg aatcgtttat tggtaacatc ttggtggctg gctagctagt ttctacagaa 1020
    31 cataatttgc ctctatagaa ggctattctt agatcatgtc tcaatggaaa cactcttctt 1080
    32 tcttagcctt acttgaatct tgcctataat aaagtagagc aacacacatt gaaagcttct 1140
    33 gatcaacggt cctgaaattt tcatcttgaa tgtctttgta ttaaactgaa ttttcttttta 1200
    34 agctaacaaa gatcataatt ttcaatgatt agccgtgtaa ctcctgcaat gaatgtttat 1260
    35 gtgattgaag caaatgtgaa tcgtattatt ttaaaaagtg gcagagtgac ttaactgatc 1320
    36 atgcatgatc cctcatccct gaaattgagt ttatgtagtc attttactta ttttattcat 1380
    37 tagctaactt tgtctatgta tatttctaga tattgattag tgtaatcgat tataaaggat 1440
    38 atttatcaaa tccagggatt gcattttgaa attataatta ttttctttgc tgaagtattc 1500
    39 attgtaaaac atacaaataa catatttaaa caaaaaaaaa aa                     1542
```

invalid <212> response. The only valid responses are DNA or RNA. For a combined DNA/RNA sequence, use <212> DNA and explain in <220>-<223> section.

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PATENT APPLICATION: **US/10/642,272**   TIME: 12:14:55

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\07072005\J642272.raw**

```
41. <210> SEQ ID NO: 2
42  <211> LENGTH: 1433
43  <212> TYPE: mRNA          same error
44  <213> ORGANISM: Rattus norvegicus
45  <400> SEQUENCE: 2
46  gctatcgtgg ctcttgcgtt ctctgaagat ggcggcagct gcgggaaggt tgctctggtc   60
47  ctcggtggct cggcctgcga gcactatttt ccggagtatt tctgcctcaa cagttcttag  120
48  gcctgttgct tctagaagaa cctgcttgac agacatgctg tggtctgcct gtccccaagc  180
49  aaagtttgcc     mark line up
50  tttagcacca gttcttcatt ccacaccct gctgtcaccc agcatgcgcc  240
51  ccattttaaa ggtactgctg ttgtcaatgg agagttcaaa gagctgagtc tcgacgactt  300
52  taaggggaaa tacttggtgc ttttcttcta ccctttggat ttcacatttg tgtgtcctac  360
53  agaaattgtt gctttcagtg acaaagccaa tgagtttcat gacgtaaact gtgaagtagt  420
54  tgcggtttct gtggattccc acttcagtca tcttgcctgg atcaacacgc caagaaagaa  480
55  tggtggtttg ggccacatga acatcacgct gttgtcggac ttaactaagc agatatcccg  540
56  agactacgga gtactgttgg aaagtgctgg cattgcgctc agaggtctct tcattattga  600
57  ccctaatggt gtcatcaagc acctgagtgt caatgacctt ccggtgggcc gaagtgtgga  660
58  agaaccactc cgtttggtaa aggcgttcca gtttgtggag acccatggag aagtctgccc  720
59  acccaactgg acaccagagt cccctacgat caagccaagt ccaacagctt caaaagagta  780
60  ctttgagaag gtccatcaat aataggtcat cctatgtctg ctggtttacc tgaagcttct  840
61  catgccaaaa gagagcccca gctggaatcc tgaagattat ttatagaatg gcaaaaacct  900
62  caccatgctt gtgtttataa gtactgctcc atgggctttg taattttaag acaggttcag  960
63  gttaaaggtg gccagctcct tccatagctg tccttactag ggacttcttg atggctacca 1020
64  attctctaca agtgcttggt ccccattct tagatcatgt cttcagaggg ttaagatttc 1080
65  ttagcctgcc ctgaagcttg gtctacagtg aagtagcaca tagcaccagt acttagtgaa 1140
66  atgaagtagc acatagcgcc agcacttagt gaaatgaagt agcatatagt gccagcactt 1200
67  agtgaaagct tctgatcaag gtcctgaaat ttcctcttgg attttgtta attatgctga 1260
68  atttcccatt attttttagt gtagtcatta actcacagtg tccttgtgtg ttctaaggta 1320
69  ttgatgagtt ataatcatga aggactatgt ttctaaaaca ctatgtcatt ttcttttctt 1380
70  caagtgctgg atgtaaagaa taaaaataaa cattaagata aaaaaaaaa aaa          1433
72  <210> SEQ ID NO: 3
73  <211> LENGTH: 1382
74  <212> TYPE: mRNA
75  <213> ORGANISM: mouse
76  <400> SEQUENCE: 3
77  ctactcctcg gtatctccgc ctatcgtgcc tcttgcgtgc tctgaagatg gcggcagctg   60
78  cgggaaggtt gctctggtcc tcggttgctc gtcatgcaag tgctatttcc cggagtattt  120
79  ctgcctcaac agttcttagg cctgttgctt ctagaagaac ctgtttgaca gacatactgt  180
80  ggtctgcctc tgcccaagga aagtcagcct ttagcaccag ttcctctttc cacacccctg  240
81  ctgtcaccca gcacgcgccc tattttaaag gtactgctgt tgtcaatgga gagttcaaag  300
82  agctgagtct cgacgacttt aagggaaaat acttggtgct tttcttctac cctttggatt  360
83  tcacatttgt gtgtcctaca gaaattgttg ctttcagtga caaagccaat gaatttcatg  420
84  atgtaaactg tgaagtagtt gcagtttcag tggattccca cttcagtcat cttgcctgga  480
85  tcaacacacc aagaaagaat ggtggtttgg gccacatgaa catcacactg ttgtcggata  540
86  taactaagca gatatcccga gactacggag tgctgttgga aagtgctggc attgcactca  600
87  gaggtctctt cattattgac cctaatggtg tcgtcaagca cctgagtgtc aacgaccttc  660
88  cggtgggccg cagtgtggaa gaaacactcc gtttggtaaa ggcgttccag tttgtagaga  720
89  cccatggaga agtctgccca gccaactgga caccagagtc ccctacgatc aagccaagtc  780
90  caacagcttc caagagtac tttgagaagg tccatcagta ggccatccta tgtctgcaat  840
```

```
 91 tacctgaagc ttttcaggcc aaaaaagagc cccagctgga atccttccaa tgccttgaag  900
 92 attatttata gaatggcaaa acctcattat gtttgtgttt ataagtactg ctccacaggc  960
 93 tttgtaattc taagacaggt tcaggctctc taaaggtggc tagctgcttc catagctgcc 1020
 94 cttactaggg acttcttggt ggctaaccaa ttctccccga gtgctttgcc cccatttctt 1080
 95 ggatcatgtc cttagagggt aagcattctt tcccttagcc tgccctgaac cttggtctac 1140
 96 agtgaagtag cacatagtgc cagtacttgg tgaaatgaag tagcacatag caccagcact 1200
 97 taatggaagc ttctgatcaa ggtcctaaaa tttcctcttg aatttttgtg aattatgctg 1260
 98 aatttccctt tttttttttt taaacagtgt ccttgtgtgt tctgaggtat tgaagaggta 1320
 99 taatcatgaa ggactatgtc taatccataa gtcattttct tcaagagctg gatatataga 1380
100 at                                                                 1382
218 <210> SEQ ID NO: 7
219 <211> LENGTH: 21
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
```

W--> 222 <220> FEATURE:
W--> 222 <223> OTHER INFORMATION: *see p.8 for error explanation*
W--> 222 <400> SEQUENCE: 7   *21⟸ per Sequence Rules, insert cumulative base total at right margin of each line*
E--> 223 tgcagtttca gtggattccc a

```
225 <210> SEQ ID NO: 8
226 <211> LENGTH: 18
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
```

W--> 229 <220> FEATURE:
W--> 229 <223> OTHER INFORMATION: *see p.8*
W--> 229 <400> SEQUENCE: 8
E--> 230 ttcatgtggc ccaaacca   *18⟸ insert*

```
232 <210> SEQ ID NO: 9
233 <211> LENGTH: 28
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
```

W--> 236 <220> FEATURE:
W--> 236 <223> OTHER INFORMATION:
W--> 236 <400> SEQUENCE: 9
E--> 237 tcttgcctgg atcaacacac caagaaag *28⟸*

```
239 <210> SEQ ID NO: 10
240 <211> LENGTH: 22
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
```

W--> 243 <220> FEATURE:
W--> 243 <223> OTHER INFORMATION:
W--> 243 <400> SEQUENCE: 10
E--> 244 ccctctgctt gctgatgtga ct   *⟸*

```
246 <210> SEQ ID NO: 11
247 <211> LENGTH: 20
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
```

W--> 250 <220> FEATURE:
W--> 250 <223> OTHER INFORMATION:
W--> 250 <400> SEQUENCE: 11

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Input Set : A:\EP.txt
Output Set: N:\CRF4\07072005\J642272.raw

```
E--> 251 cctgtaagcg atgccctcat
     253 <210> SEQ ID NO: 12
     254 <211> LENGTH: 29
     255 <212> TYPE: DNA
     256 <213> ORGANISM: Artificial Sequence
W--> 257 <220> FEATURE:
W--> 257 <223> OTHER INFORMATION:
W--> 257 <400> SEQUENCE: 12
E--> 258 agcttgtccc agaattacgg cgtgttgaa
     260 <210> SEQ ID NO: 13
     261 <211> LENGTH: 19
     262 <212> TYPE: DNA
     263 <213> ORGANISM: Artificial Sequence
W--> 264 <220> FEATURE:
W--> 264 <223> OTHER INFORMATION:
W--> 264 <400> SEQUENCE: 13
E--> 265 gcggatgaag agaggcatg
     267 <210> SEQ ID NO: 14
     268 <211> LENGTH: 18
     269 <212> TYPE: DNA
     270 <213> ORGANISM: Artificial Sequence
W--> 271 <220> FEATURE:
W--> 271 <223> OTHER INFORMATION:
W--> 271 <400> SEQUENCE: 14
E--> 272 gccacaccgt cctttcca
     274 <210> SEQ ID NO: 15
     275 <211> LENGTH: 23
     276 <212> TYPE: DNA
     277 <213> ORGANISM: Artificial Sequence
W--> 278 <220> FEATURE:
W--> 278 <223> OTHER INFORMATION:
W--> 278 <400> SEQUENCE: 15
E--> 279 tggagacctg ggcaatgtgg ctg
     281 <210> SEQ ID NO: 16
     282 <211> LENGTH: 17
     283 <212> TYPE: DNA
     284 <213> ORGANISM: Artificial Sequence
W--> 285 <220> FEATURE:
W--> 285 <223> OTHER INFORMATION:
W--> 285 <400> SEQUENCE: 16
E--> 286 acgggtgctc agcctcc
     288 <210> SEQ ID NO: 17
     289 <211> LENGTH: 18
     290 <212> TYPE: DNA
     291 <213> ORGANISM: Artificial Sequence
W--> 292 <220> FEATURE:
W--> 292 <223> OTHER INFORMATION:
W--> 292 <400> SEQUENCE: 17
E--> 293 aggcttgtgc cctgcttc
```

```
         295 <210> SEQ ID NO: 18
         296 <211> LENGTH: 25
         297 <212> TYPE: DNA
         298 <213> ORGANISM: Artificial Sequence
W--> 299 <220> FEATURE:
W--> 299 <223> OTHER INFORMATION:
W--> 299 <400> SEQUENCE: 18
E--> 300 cagcctgcac tgaggagatc cctca
         302 <210> SEQ ID NO: 19
         303 <211> LENGTH: 28
         304 <212> TYPE: DNA
         305 <213> ORGANISM: Artificial Sequence
W--> 306 <220> FEATURE:
W--> 306 <223> OTHER INFORMATION:
W--> 306 <400> SEQUENCE: 19
E--> 307 aaccgcggtc gtggctcttg cgttctct
         309 <210> SEQ ID NO: 20
         310 <211> LENGTH: 30
         311 <212> TYPE: DNA
         312 <213> ORGANISM: Artificial Sequence
W--> 313 <220> FEATURE:
W--> 313 <223> OTHER INFORMATION:
W--> 313 <400> SEQUENCE: 20
E--> 314 gcgctagctt attgatggac cttctcaaag
         316 <210> SEQ ID NO: 21
         317 <211> LENGTH: 20
         318 <212> TYPE: DNA
         319 <213> ORGANISM: Artificial Sequence
W--> 320 <220> FEATURE:
W--> 320 <223> OTHER INFORMATION:
W--> 320 <400> SEQUENCE: 21
E--> 321 ttacagattg ccgcctgctc
         323 <210> SEQ ID NO: 22
         324 <211> LENGTH: 20
         325 <212> TYPE: DNA
         326 <213> ORGANISM: Artificial Sequence
W--> 327 <220> FEATURE:
W--> 327 <223> OTHER INFORMATION:
W--> 327 <400> SEQUENCE: 22
E--> 328 ccagcagtgg aataaggcct
         330 <210> SEQ ID NO: 23
         331 <211> LENGTH: 25
         332 <212> TYPE: DNA
         333 <213> ORGANISM: Artificial Sequence
W--> 334 <220> FEATURE:
W--> 334 <223> OTHER INFORMATION:
W--> 334 <400> SEQUENCE: 23
E--> 335 aatcacgacc cactgcaagg aacca
         337 <210> SEQ ID NO: 24
```

```
RAW SEQUENCE LISTING               DATE: 07/07/2005
PATENT APPLICATION:  US/10/642,272   TIME: 12:14:55

          Input Set : A:\EP.txt
          Output Set: N:\CRF4\07072005\J642272.raw
```

```
        338 <211> LENGTH: 19
        339 <212> TYPE: DNA
        340 <213> ORGANISM: Artificial Sequence
W--> 341 <220> FEATURE:
W--> 341 <223> OTHER INFORMATION:
W--> 341 <400> SEQUENCE: 24
E--> 342 tgcaccacca actgcttag
        344 <210> SEQ ID NO: 25
        345 <211> LENGTH: 19
        346 <212> TYPE: DNA
        347 <213> ORGANISM: Artificial Sequence
W--> 348 <220> FEATURE:
W--> 348 <223> OTHER INFORMATION:
W--> 348 <400> SEQUENCE: 25
E--> 349 ggatgcaggg atgatgttc
        358 <210> SEQ ID NO: 27
        359 <211> LENGTH: 877
E--> 360 <212> TYPE: mRNA
        361 <213> ORGANISM: Rattus norvegicus
W--> 362 <400> SEQUENCE: 27
        363 gaattcggca cgagggtcgt ccgcgtgtcc ggctcttgcc cacgcagtca tggcctccgg   60
        364 caacgcgcac atcggaaagc ctgcccctga cttcacgggc accgccgtgg tggatggtgc  120
        365 ctttaaggaa atcaagcttt cagactacag agggaagtac gtggtcctct ttttctatcc  180
        366 actggacttc acttttgttt gccccacgga gatcatcgct tttagcgacc acgctgagga  240
        367 cttccgaaag ctaggctgcg aggtgctggg agtgtctgtg gactctcagt tcacccacct  300
        368 ggcctggatc aataccccac ggaaggaggg aggcttgggc ccactgaata tccctctgct  360
        369 tgctgatgtg actaaaagct tgtcccagaa ttacggcgtg ttgaaaaatg atgagggcat  420
        370 cgcttacagg ggcctcttta tcatcgatgc caagggtgtc cttcgccaga tcacagtcaa  480
        371 cgacctacct gtgggacgct ctgtagatga ggctctccgc ctcgtccagg cctttcagta  540
        372 tacagatgag catggggaag tctgtcctgc tggctggaag cccggcagtg acaccatcaa  600
        373 acccaatgtg gatgacagca aggaatactt ctccaaacac aactgagatg ggtaaacatc  660
        374 ggtgagcctg aatcccggat ctcacctgcg cccttacctg gatgtcctgt gctggcccag  720
        375 aaaacgctag atcttcctct acattctaaa ggggctggag gctaggccga ggctttctca  780
        376 ttacccacct ggaatctggt gaatagtgac cctgccctga gcacacccag ctgggcccag  840
        377 gtctatagga aaccaataaa gtattaggga cagtgta                            877
        411 <210> SEQ ID NO: 29
        412 <211> LENGTH: 560
E--> 413 <212> TYPE: mRNA
        414 <213> ORGANISM: Homo sapiens
W--> 415 <400> SEQUENCE: 29
        416 atggcgacga aggccgtgtg cgtgctgaag ggcgacggcc cagtgcaggg catcatcaat   60
        417 ttcgagcaga aggaaagtaa tggaccagtg aaggtgtggg gaagcattaa aggactgact  120
        418 gaaggcctgc atggattcca tgttcatgag tttggagata atacggcagg ctgtaccagt  180
        419 gcaggtcctc actttaatcc tctatccaga aaacacggtg ggccaaagga tgaagagagg  240
        420 catgttggag acttgggcaa tgtgactgct gacaaagatg gtgtggccga tgtgtctatt  300
        421 gaagattctg tgatctcact ctcaggagac cattgcatca ttggccgcac actggtggtc  360
        422 catgaaaaag cagatgactt gggcaaaggt ggaaatgaag aaagtacaaa gacaggaaac  420
        423 gctggaagtc gtttggcttg tggtgtaatt gggatcgccc aataaacatt cccttggatg  480
        424 tagtctgagg cccccttaact catctgttat cctgctagct gtagaaatgt atcctgataa  540
```

FYI: same error in Sequence 26

RAW SEQUENCE LISTING   DATE: 07/07/2005
PATENT APPLICATION: **US/10/642,272**   TIME: 12:14:55

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\07072005\J642272.raw**

425 acattaaaca ctgtaatctt   560

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/07/2005
PATENT APPLICATION: US/10/642,272   TIME: 12:14:56

Input Set : **A:\EP.txt**

error Explanation ·Output Set: **N:\CRF4\07072005\J642272.raw**

Use of <220> Feature(NEW RULES):

Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is **MANDATORY** if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26

VERIFICATION SUMMARY   DATE: 07/07/2005
PATENT APPLICATION: **US/10/642,272**   TIME: 12:14:56

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\07072005\J642272.raw**

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:7 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:43 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:190 SEQ:2
L:74 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:76 M:283 W: Missing Blank Line separator, <400> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:144 M:283 W: Missing Blank Line separator, <400> field identifier
L:183 M:283 W: Missing Blank Line separator, <400> field identifier
L:222 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:222 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:222 M:283 W: Missing Blank Line separator, <400> field identifier
L:222 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:222
L:223 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:7
L:229 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:229 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:229 M:283 W: Missing Blank Line separator, <400> field identifier
L:229 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:229
L:230 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:8
L:236 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:236 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:236 M:283 W: Missing Blank Line separator, <400> field identifier
L:236 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:236
L:237 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:9
L:243 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:243 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:243 M:283 W: Missing Blank Line separator, <400> field identifier
L:243 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:243
L:244 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:10
L:250 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:250 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:250 M:283 W: Missing Blank Line separator, <400> field identifier
L:250 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:250
L:251 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:11
L:257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial Sequence
L:257 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>

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ORGANISM:Artificial Sequence
L:257 M:283 W: Missing Blank Line separator, <400> field identifier
L:257 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:257
L:258 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:12
L:264 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:264 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:264 M:283 W: Missing Blank Line separator, <400> field identifier
```

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PATENT APPLICATION: **US/10/642,272**   TIME: 12:14:56

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\07072005\J642272.raw**

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L:264 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:264
L:265 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:13
L:271 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:271 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:271 M:283 W: Missing Blank Line separator, <400> field identifier
L:271 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:271
L:272 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:14
L:278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:278 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:278 M:283 W: Missing Blank Line separator, <400> field identifier
L:278 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:278
L:279 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:15
L:285 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:285 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:285 M:283 W: Missing Blank Line separator, <400> field identifier
L:285 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:285
L:286 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:16
L:292 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:292 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:292 M:283 W: Missing Blank Line separator, <400> field identifier
L:292 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:292
L:293 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:17
L:299 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:18, <213>
ORGANISM:Artificial Sequence
L:299 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:18, <213>
ORGANISM:Artificial Sequence
L:299 M:283 W: Missing Blank Line separator, <400> field identifier
L:299 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:299
L:300 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:18
L:306 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:306 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:306 M:283 W: Missing Blank Line separator, <400> field identifier
L:306 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:306
L:307 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:19
L:313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:313 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:313 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:313
L:314 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:20
L:320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
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L:320 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:320 M:283 W: Missing Blank Line separator, <400> field identifier
L:320 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:320
L:321 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:21
L:327 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:327 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:327 M:283 W: Missing Blank Line separator, <400> field identifier
L:327 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:327
L:328 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:22
L:334 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:334 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence

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Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\07072005\J642272.raw**

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L:334 M:283 W: Missing Blank Line separator, <400> field identifier
L:335 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:23
L:341 M:283 W: Missing Blank Line separator, <400> field identifier
L:342 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:24
L:348 M:283 W: Missing Blank Line separator, <400> field identifier
L:349 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:25
L:355 M:283 W: Missing Blank Line separator, <400> field identifier
L:356 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:26
L:360 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:362 M:283 W: Missing Blank Line separator, <400> field identifier
L:383 M:283 W: Missing Blank Line separator, <400> field identifier
L:413 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:415 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:283 W: Missing Blank Line separator, <400> field identifier
```